Perfect score:

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Scoring table:

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Mouse spliced transcript detection oligonucleotide SEQ ID NO:24971
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                                                        AAZ 67790
ABN47816
AAL30269
ABN39375
ABN28030
AAAL1650
ABL46029
AAN80654
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ABL45019
AAL29070
AAC23790
AAT97276
ABN28389
AAL30738
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AAT78604
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ABN44442
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AAA75934
AAH22252
AAH20117
AAV70103
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ABN32873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN52223 standard; DNA; 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COMP-) COMPUGEN INC
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splice
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CFTR binding site
Human spliced tran
Human map-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HER2 partial
Human spliced tran
Human SNP flanking
Human spliced tran
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(without alignments)
13063.385 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                             tgagcaccagccaaccaggg............1atgaaacactaaaaaaaa 1456
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:
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                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM nucleic - nucleic search, using sw model
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ABN49410
AAZ66146
AAZ65699
AAA73834
ABN40794
                                                                                                                               October 31, 2002, 19:48:26
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 75
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Human coding sequ Human spliced tran Human spliced tran 5-enolpyruvylshiki Special AT rich (A Human coding sequ Human spliced tran

SNP oligonuc secreted pro

Human Human

chromosome

Human

SELEX-derived n Class I SELEX g Human chorionic spliced

VH and scFv antibo Human spliced tran Human spliced tran

tran nucl gene chorionic go

Human

Human spliced tran Rat spliced transc Humanised anti-Fas

Human

Humanised anti-Fas Human map-related Human SNP oligonuc

probe used

75-mer

Rat spliced transc SNP oligonuc Human map-related Human spliced tran SNP oliqonuc

Nucleotide EP-13

Rabbit anti A33 an Humanised HFE7A he Allelic ladder, HU

New oligonucleotide libraries comprising oligonucleotides which. selectively hybridize to mRNAs transcribed from a transcription unit of

AAH38784 ABN39098

31.4 27.8 27.6 26.2 26.2 25.8 25.8 25.4 25.4

Score 45

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Result

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Human reproductive PCR primer used to -A33 antigen a

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Only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN77253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N. B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cystic fibrosis transmembrane conductance regulator; CFTR; gene therap protein binding site; nuclear extract; gene promoter; cystic fibrosis; spatial expression regulator; CF; ss.
                                                                                    The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1017 GACCTCTTCTTCGCCCTATCATTGGAGATGTTGACATCGCTGGCCTTCTTGGGGACATG 1076
                                                                                                                                          transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively obtained that the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries and splice variants of human or animal transcriptomes. The libraries of a sub-transcriptome under a particular biological or pathological state, and so allowing the particular biological or pathology specific genes such as these genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 24; Length 65;
Pred. No. 0.004;
0; Mismatches 10; Indels
useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 15 A; 18 C; 14 G; 18 T; 0 other;
                                                      Example 1; SEQ ID 24971; 47pp; English.
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illarity 83.6%;
Conservative 0
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                      developmental specific genes
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SISI (-SISI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT89492;
            genome,
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proteins found in the nuclear extracts of cystic fibrosis transmembrane conductance regulator (GFTR)-expressing cells. This sequence is an oligonuclectide of the invention. This sequence, and sequences containing the increase the activity of the CFTR gene promoter, so regulate spatial expression of this gene (unlike viral or other promoters used in gene therapy). Constructs containing this sequence are used in gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcribtome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription units that populate a genome. The library comprises transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                    New oligo:nucleotide(s) for gene therapy of cystic fibrosis - are able to increase the activity of the CF trans-membrane conductance regulator gene promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse; rat; splice transcript; detection; RNA transcript;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557 AAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATT 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49 BP; 15 A; 10 C; 5 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31.4; DE Pred. No. 32; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID 22158; 47pp; English.
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                                                                                                                                                                                                                                         Claim 3; Page 16; 20pp; English.
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02-MAY-2001; 2001US-287724P.
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nilarity 77.6%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cystic fibrosis (CF).
WPI; 1997-480211/44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200210449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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ABN49410/c
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biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in a detection RNA transcripts and splice variants of human or animal transcripts and splice variants of human or animal transcripts on detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathological state, and so allowing the detection of tissue- and pathology specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN2723 to ABN59589 represent coligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N. B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60 BP; 10 A; 14 C; 16 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
             555555555555555555588888
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Gaps
                              ö
    DB 24; Length 60;
Score 27.8; DB 24; Length (Pred. No. 4e+02; O; Mismatches 17; Indels
  1.9%;
             st Local Similarity 69.1
tches 38; Conservative
  ery Match
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RESULT 4 AAZ66146/c

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AAZ66146 standard; DNA; 47

AAZ66146;

(first entry) 10-SEP-2001

Human map-related biallelic marker SEQ ID NO:493.

Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNR; ds.

Homo sapiens

Location/Qualifiers replace(24,G) Key variation

/*tag= a /standard_name= "single nucleotide polymorphism"

WO9954500-A2

28-OCT-1999

99WO-IB00822. 21-APR-1999;

98US-0082614 98US-0109732 21-APR-1998; 23-NOV-1998;

(GEST) GENSET

Chumakov I; Cohen D, Blumenfeld M,

WPI; 2000-013267/01

Novel biallelic markers used to construct a high density disequilibrium map of the human genome

Claim 1; Page 335; 2745pp; English.

AA265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences: AAZ69579 to AAZ77440 represent amplification

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Novel biallelic markers used to construct a high density disequilibrium
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primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also
                                                                                                                                                                                                                                                      effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                  be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                            N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human map-related biallelic marker SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554 ATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 47 BP; 15 A; 9 C; 11 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27.6; DB 2
Pred. No. 4e+02;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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y 78.68;
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                                                                                                                                                                                                                                                                                                                                                                         from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Local Sim.
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                                                                                                                                                                                                                                                                                      treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present sequence comprises a fragment of the human her2 oncogene. It was used with fragments of the human chorionic gonadotrophin (hCG) beta-subunit cDNA to create a fusion molecule, which could then be used
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haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= sticky_end
/note= "Also, the 5' end of the complementary strand
overhangs the 3' end of this strand by the sequence
5'-AA-3'"
                                                                                                                            N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.
                                                                                                                                                                                                                                        Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; choriònic gonadotrophin; hCG; DNA vaccine; cancer; fertility control; contraceptive; immunogen; her2; ds.
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                        Score 26.2; DB 21;
Pred. No. 1e+03;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                               550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAA 588
                                                                                                                                                                                                                                                                                                                                    BP; 17 A; 10 C; 11 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HER2 partial coding sequence #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA73834 standard; DNA; 73 BP.
                                                                                                                                                                                                                                           1.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                Similarity
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misc_feature
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                                                                                                                                                                                                         Sequence 47
                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                           Query Match
Best Local Si
                                                                                                                      treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA73834;
                                                                                                                                                                                                                                                                                   Matches
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AAA73834
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in the methods of the invention which involve the use of DNA vaccines encoding hCG antigens to induce an immune response and enable the treatment of cancer and provide a novel method of fertility control. In particular, they can be used to treat colorectal, breast and lung cancer as hCG is associated with these types of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcriped from a given transcription unit of the genome, which encodes one or more; messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a configuration of the configuration 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGCCAAGACAGTGGCCTTCCTCAGGAACCTGCCATCCTTCTGGCAGCTGCCTCCCCAG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qualitatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quantitatively characterising the corresponding transcriptome, and detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub_transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human spliced transcript detection oligonucleotide SEQ ID NO:13542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; rat; splice transcript; detection; RNA transcript;
splice variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                  Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         blological sample, in expression profiling studies, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Faigler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                       Sequence 73 BP; 19 A; 24 C; 19 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 21;
Pred. No.*1.5e+03;
0; "Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mintz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID 13542; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mintz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN40794 standard; DNA; 60 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a genome, useful for detectir
developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000US-221607P. 02-MAY-2001; 2001US-287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2001; 2001WO-IB01903.
                                                                                                                                                                                                                                                                                                                                                                                         1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 62.1
es 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 GACCAG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200210449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAAG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN40794;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7. ABN40794/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
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                                         SSSSSX8
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only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent.
                                                                                                                                                                                                                                                                           the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                 Oligonucleotide sequences from rats, humans and mice, which are used in
                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
Fri
                                                                                                                                           888888888888888
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Sequence 60 BP; 16 A; 15 C; 11 G; 18 T; 0 other;

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Gaps
                   ;
0
Score 25.8; DB 24; Length 60;
Pred. No. 1.5e+03;
0; Mismatches 12; Indels
                                   1.8%;
                   33; Conservative
 Ouery Match
Best Local Similarity
                   Matches
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AAH38784 standard; DNA; 47 BP

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AAH38784;

(first entry)

14-AUG-2001

Human SNP flanking oligonucleotide SEQ ID 1580.

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; ds.

Homo sapiens

WO200129262-A2

26-APR-2001

99US-0160096 15-OCT-1999; (ORCH-) ORCHID BIOSCIENCES INC

Pohl M; Picoult-Newburg L,

WPI; 2001-290930/30

New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic acid sample

Claim 1; Page 58; 83pp; English

primer extension (SNPD primers, entry plimers, suiter uncrective primer extension (SNPD primers, entry primers, entry consider the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyphing primer. For oligonucleotides are useful for genotyphing a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotypic of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide

transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a

biological sample, in expression profiling studies, in qualitatively quantitatively characterising the corresponding transcriptome, and indetecting RNA transcripts and splice variants of human or animal

transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the

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                                                                                                     pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes oligonucleotide libraries for detecting messenger RNAs that bobulate a (sub-)transcriptome, where the
                                                                                                                                    present sequence represents a fragment of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
              dýstrophy, familial hypercholesterolaemia, polycýstic Kidney disease, osteogenesis imperfecta and acute intermittent porphyrla. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inclidance, necessay, such as system diseases and infection by pathog microorganism. The method is also useful in forensic investigations an
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human spliced transcript detection oligonucleotide SEQ ID NO:11846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; rat; splice transcript; detection; RNA transcript;
splice variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                      Length 47;
                                                                                                                                    paternity analysis. The present sequence represents a frac
DNA flanking the site of a single nucleotide polymorphism
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Faigler
                                                                                                                                                                                                                                                                                                            4 AGAGGTCCAGCCACTTGCCCAAGGCCACACACGCTCTTATTTGA 46
                                                                                                                                                                                                                    Score 25.4; DB 22;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                        550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGA
                                                                                                                                                                                      Sequence 47 BP; 12 A; 15 C; 11 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mintz E, Mintz L,
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID 11846; 47pp; English
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                             ABN39098 standard; DNA; 60 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2001; 2001WO-IB01903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                                                                                                                                                                                                                                      74.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-257383/30.
                                                                                                                                                                                                                                     Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200210449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN39098;
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                             ABN39098/c
                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
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Rat spliced transcript detection oligonucleotide SEQ ID NO:1137

(first entry)

15-JUL-2002

ABN28389;

ABN28389 standard; DNA; 65 BP.

ABN28389/c RESULT 11

Human; mouse; rat; splice transcript; detection; RNA transcriptione; oligonucleotide library; ss

Rattus norvegicus

WO200210449-A2.

37-FEB-2002.

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Faigler

Mintz; L,

Wasserman A, Mintz E,

Shoshan A,

28-JUL-2000; 2000US-221607P. 32-MAX-2001; 2001US-287724P. 20-JUL-2001; 2001WO-IB01903

02-MAY-2001;

COMP-) COMPUGEN INC.

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detection of itssue- and pathology specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N. B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a nucleotide sequence from example 7 of the present invention describing a HCV chimeric peptide antigen which comprises at least 2 peptide epitope regions from the HCV polypeptide core region, 2 peptide epitope regions from the NS3 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections with high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and at least 2 peptide epitope regions from the NS4 region. The anti-
binds specifically with an antibody produced by a human infected by
HCV. The peptide can detect a wide range of HCV infections with high
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide antigen derived from hepatitis C virus protein detecting HCV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; chimeric; antigen; detection; core region; epitope; NS3; NS4; infection; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1081 TGCTCAGGTGACCTGTTCCAGCCCAGGCAGAGATCAGGTGGGCAGAGGCTG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 72;
                                                                                                                                                                                                                                Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                   Score 25.4; DB 24; Length Pred. No. 2e+03; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide EP-13 SEQ ID NO:51 from J09278794 Example 7.
                                                                                                                                                                                                                                                                                                       604
                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.4; DB 19;
Pred. No. 2.2e+03;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 72 BP; 15 A; 25 C; 21 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                       562 ACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGAT
                                                                                                                                                                                                                                                                                                                         BP; 14 A; 16 C; 15 G; 15 T; 0 other;
                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; page 14; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
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milarity 68.6%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAT97276 standard; DNA; 72 BP
                                                                                                                                                                                                                                  1.7%;
illarity 74.4%;
conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0027015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96JP-0024045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-022248/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best<sup>-</sup>Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                         Local Similarity
nes 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1997
                                                                                                                                                                                                      Sequence 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP09278794-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT97276:
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               AAT97276/C
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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                22222222222222<u>x</u>8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribted from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humans and mice, which are used in
                                                                                                                                                                                                                                                                describes oligonucleotide libraries for detecting
                                          New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue", pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathology-specific genes such as those genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quantitatively characterising the corresponding transcriptome, and detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from a particular disorder, ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    707 AGGAGGAGGTAGTAGTĞGGACCTCAAAGGCCĞAGCAAAGGAGGAG 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65 BP; 8 A; 23 C; 14'G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25.2; DB 24
Pred. No. 2.4e+03;
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                            Example 1; SEQ ID 1137; 47pp; English;
                                                                                                                      a genome, useful for detecting
developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection of tissue- and
                                                                                                                                                                                                                                                                                 invention
WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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ōλ

ŏ qq. /*tag= a /standard_name= "single nucleotide polymorphism"

Location/Qualifiers

Homo sapiens

colony stimulating factor;

amylase; cancer; .n; cadherin;

replace(24,G)

variation

W09954500-A2

biallelic marker; high density disequilibrium map

denome;

Human

Human map-related biallelic marker SEQ ID NO:2137

(first entry)

10-SEP-2001

AAZ67790;

AAZ67790 standard; DNA; 47 BP

genomic map; haplotype; phenotype; polymorphic base; genotypin haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.

genotyping

RESULT 12

```
(e.g. cancers of the bladder, brain, breast, colon and kidney,
leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amplases, amyloid proteins, anglopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins, cytochromes, kinesins, cytokhnes, interferons, interleukins, of protein coupled receptors and thioesterases. The present sequence is, one such oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer
                                                                                                                                                                                                                                                            neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; andlopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating fact complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation;
                                                                                                                                                                                                                                            antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25, DB 22; Length 51
Pred. No. 2.4e+03;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and cancer, autoimmune diseases and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51 BP; 13 A; 5 C; 1 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g. cancers of the bladder, brain, breast,
                                                                                                                                                                                                                                            Immunosuppressive; immunostimulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 2520; 4143pp; English
                                                                                                                                                                                   Human SNP oligonucleotide #3946.
                             AAL30738 standard; DNA; 51 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2000; 2000WO-US35498
                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disease; ss
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                 multifactorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200147944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA,
                                                                                                                                  24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2001
                                                                                 AAL30738;
AAL30738,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62888888888888
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polymerases,

cyclins, p treating,

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Gaps
             N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing
                                                                                                                                                   ;
0
                                                                                                                  Length 47;
                                                                                                                                                 Indels
                                                                                                                                                                                                     3 AGAAACAAGGAGACTTGCCCAAGGTCGTGCATCAATTAAGTGCC 46
                                                                                                                                                                                  550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGAC
                                                                                                                21;
                                                                              Sequence 47 BP; 16 A; 10 C; 11 G; 10 T; 0 other;
                                                                                                                Score 24.8; DB 21
Pred. No. 2.6e+03;
                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                 ABN47816 standard; DNA; 60 BP
                                                                                                                1.78;
72.78;
                                              from the present invention
                                                                                                                                                 Conservative
                                                                                                                                Similarity
treatment.
                                                                                                               Query Match
                                                                                                                                   Local
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                   ABN47816
ID ABN4
XX
AC ABN4
                                                                                                                                                                                    δy
                                                                                                                                                                                                                Q
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ö

Gaps

Length 51;

al Similarity 69.4%; 34; Conservative

Query Match Best Local Similarity

Matches

õ g

49

RESULT 13

AA267790

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characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ65654 to AAZ69578 represent human biallelic markers from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ6579 to AAZ7440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: They can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies. Which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side
                                                                                                                                                                                                                                                                                                                                                    Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 686; 2745pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel biallelic markers used
                                                                    99WO-IB00822.
                                                                                                                                                    98US-0082614.
                                                                                                                                                                                                                                                                                                                                                Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            map of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                        21-APR-1999;
                                                                                                                                                    21-APR-1998;
23-NOV-1998;
28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                    Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN47816
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(COMP-) COMPUGEN INC
                 Human;
XX
XX
XX
XX
XX
XX
XX
YX
YX
YX
YX
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Human spliced transcript detection oligonucleotide SEQ ID NO:20564.
                                                                                 splice transcript; detection; RNA transcript;
                                                                                                  splice variant; transcriptome; oligonucleotide library; ss
                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                                                                                                                                                                                                                                                                          2001WO-IB01903.
(first entry)
                                                                                            rat;
                                                                                                                                                                                            WO200210449-A2
                                                                                          mouse;
                                                                                                                                                                                                                                                                            20-JUL-2001;
                                                                                                                                                        Homo sapiens
    15-JUL-2002
                                                                                                                                                                                                                                     07-FEB-2002.
```

New oligonuclectide libraries comprising oligonuclectides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and Faigler S; Mintz L, Mintz E, developmental-specific genes Wasserman·A, WPI; 2002-257383/30.. Shoshan A,

Example 1; SEQ ID 20564; 47pp; English

only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profilling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal invention describes oligonucleotide libraries for detecting transcriptomes. The libraries may also be used as specialised mini-libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes ftp.wipo.int/pub/published_pct_sequences present

Sequence 60 BP; 20 A; 13 C; 15 G; 12 T; 0 other;

601 . 0 Length 60; Indels DB 24; Score 24.6; DB 24 Pred. No. 3.5e+03; 0; Mismatches y Match 1.7%; Local Similarity 65.5%; hes 36; Conservative Query Match Best Local 3 Matches δŻ

55 547 CCCAGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGG

AAL30269/C ID AAL30269 standard; DNA; 51 BP

RESULT 15

g

AAL30269;

(first entry) 24-JAN-2002 Human SNP oligonucleotide #3477.

amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; Grprotein coupled receptor; thioesterase; inflammation; Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; disease; "autoimmune disease; infection nervous system disease; ss multifactorial

Homo sapiens.

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US35498

28-DEC-1999; 99US-0173419. 27-DEC-2000; 2000US-0173419.

Leach Shimkets RA,

(CURA-) CURAGEN CORP.

WPI; 2001-465210/50.

cyclins, polymerases Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymoncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections

Claim 1; Page 2383; 4143pp; English

(e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytchromes, kinaseins, cytchromes, interferons, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer organisms

Sequence 51 BP; 12 A; 1 C; 2 G; 36 T; 0 other;

Gaps . 0 Length 51; Indels Score 24.4; DB 22; Pred. No. 3.6e+03; 0; Mismatches 16; 0; 1:78; 68.08; Query Match
Best Local Similarity 68.0'

g

Search completed: October 31, 2002, 21:55:33 Job time: 253 secs

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GenCore version 5.1.3 . Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM nucleic - nucleic	ic search, using sw model	
Run on: Oc	October 31, 2002, 19:54:31; Search time 2921 Seconds (without alignments) 14506.568 Million cell updates/sec	ec
Title: US Perfect score: 14 Sequence:	US-09-919-197-3 1456 1 tgagcaccagccaaccagggtatgaaacactaaaaaaa 1456	
Scoring table: ID	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched: 20	2054640 seqs, 14551402878 residues	
l number of hi	hits satisfying chosen parameters: 941340	
Minimum DB seq len Maximum DB seq len	length: 0 length: 75	
Post-processing: M	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : Grand Part Part Part Part Part Part Part Part	GenEmbl:* gb_ba:* gb_ln:* gb_ln:* gb_ln:* gb_pa::* gb_pa::* gb_pa::* gb_pp::* gb_pp::*	
- 41	:: em_htgo_other:*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

٠.		Description	31 Sequence 2		57 Se	E1419/ PCR primer	AJUU1623 HOMU Sapi E40916 Humanized a		AR117953 Sequence	. 79		m		A08223 Synthetic O	AJ345111 Carping	82 Sequenc				S	Ω.		AX002002 Sequence		Human	Hn		ARII/040 Sequence	T20500 Sequence	Sequence	20 Constru	Φ	41	ń	140677 Sequence 23	Sequence	89442 Sequence	X328443 Sequence	0	3353 Se	NA e		
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1											•																													-	
SUMMARIES		ID	A65431	m	AX116457	E1419/	vi	A05173	35	9		AR066039	A15067	AUG223	CBE345111	AX199582	AX482787	AX199690	AR139994	AX485185	AK184251	AX107963	AX002002	E40050	E40858		AR051730	AKII/040	120500	I49676	BD002020	108751	AR117041	AR200054	1,0677	7668	944	AX328443	54	35	E03095	2	
		th DB	49 6	7		-	5.4 5.4 5.4	· LC	0		Д.		75.0	# T	74 . 8	0	5	0	4		000	οα	വ	ı.		2	, (+	O T O	4	ı 1	3		s i	ما	ר ער	nσ	, 0	0	6	-	58 6	D.	•
	* Query	Match Length	2.2	2.0	1.7	۱. ر ا	, ,	9.1	1.6	1.6	1.6	1.6	1.6 1.6	9.4	1.6	1.6	1.6	1.5	1.5	٠. د د	L. 1.	. r.	1.5	1.5	1.5	1.5	٠. دی	٦ - د د		1.5	1.5	1.5	•	۲.5 ت			1.5		1.5	1.5	1.5	1.5	
	~ ā	Score Ma	31.4	29.4	25.4	4.07	23.8	23.6	23.6	23.6	23.6	23.6	۳,	0 60	5.	2	22.6	22.4	22.4	22.4	27.7	22.22	22.2	22.2	22.2	22.2	22.2	2.22	22.2	22.2	22.2	22.2	22.2	22.2	4	22.22	22.2		~	22	.22	22	
•	Result	No.	-		ო •	4. rt	n ve		80	•		Н,	75	4 -	15	16	17	Η.		2 (77	7 6	1 (1	(7	36	7		7 (ייי נ	m	٣	34	32	3.6	- a) (r	4	4	42	4	44	45	
	Re		υ	O		J				υ	O	υ	O) U				υ				ပ				OI			, 0	υ	,				C	, O				O	J	

A65431
Sequence 23 from Patent W09735005.
A65431
A65431
GI:4531190
unidentified
unclassified.
1 (bases 1 to 49)

RESULT 1
A65431/c
LOCUS
DEFINITION OF ACCESSION VERSION KEYWORDS
SOURCE
ORGANISM

PAT 29-MAR-1999

linear

ALIGNMENTS

REFERENCE 1 (bases 1 to 49)
AUTHORS Harris, A.
TITLE CFTR GENE REGULATOR
JOURNAL PATENT: NO 9735005-A 23 25-SEP-1997;
ISIS INNOVATION (GB)

PAT 28-JUL-1999

source

FEATURES

COMMENT

BASE COUNT

ORIGIN

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HS001823 64 bp DNA linear PRI 30-SEP-1997
Homo sapiens exon 2E4 from Los Alamos contig C159.1, chromosome
16p12.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HASEGAWA AKIRA
CO7K14/18, C07H21/04, C07K19/00, C12N15/09, C12P21/02, G01N33/53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamaguchi,K., Kashiwaguma,T., Chiba,Y., Yagi,S. and Hasegawa,A.
CHIMERA ANYIGEN PEPTIDE
Patent: JP 1997278794-A 40 28-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAMAGUCHI KENJIRO, KASHIWAGUMA TOMIKO, CHIBA YUKIE, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pc c12N1/21, (c12P21/02, c12R1:19), (c12N1/21, C12R1:19); CC strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Artificial sequences'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 72;
                                                                                                                    Length 47
                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                     72 bp DNA lines
PCR primer for gaining C7 region epitope of HCV.
E14197
                                                                                                                                                                                                                      Score 25.4; DB 6;
Pred. No. 8.7e+04;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                    %; Score 25.4; DB 6;
%; Pred. No. 8.1e+04;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unidentified"
/db_xref="taxon:32644"
/25 c 21 g 11
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-1997 JP 1997027015
09-FEB-1996 JP 96P 240
                                                          11 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:2462356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP 1997278794-A/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.78;
68.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E14197.1 GI:5708880
JP 1997278794-A/40.
                                                                                                                               Query Match 1.7%;
Best Local Similarity 74.4%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 68.6
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 72)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAM 16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evolutionary inventions and continuity of CORE-SINEs in mammals J. Mol. Biol. 298 (3), 365-377 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529 CCGATAAAGAAACTGAAGCCCAGA-GATTAAGTGACTTGCCCAAGGTCACCCAGCTAAT 586
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Didelphis virginiana isolate O51 retroposon CORE-SINE Mar-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29.4; DB 4; Length 71; Pred. No. 6.9e+03; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Didelphimorphia; Didelphidae;
                                                                                                                                                                                                                                                                                                                           557 AAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="retroposon CORE-SINE Mar-1"
/rpt_type-dispersed
19 c 15 g 23 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                        49 AAGTAAATTGCCTAAGATCACATTGTTAATAAGTGACAGAGTAGGATT 1
                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l. 71
/orqanism="Didelphis virginiana"
                                                                                                                                                                                                                         Score 31.4; DB 6;
Pred. No. 1.8e+03;
0; Mismatches 11;
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                          publication AU 2036897 19971010.
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                                                                               1. .49
/organism="unidentified"
/db_xref="taxon:32644"
a 10 c 5 g 1
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1. .71
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Gilbert, N. and Labuda, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /isolate="051"
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Local Similarity 79.7%;
nes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Didelphis virginiana.
                                                                                                                                                                                                                            Query Match 3 2.2%;
Best Local Similarity 77.6%;
Matches 38; Conservative
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Oligonucleotide probe corresponding to the CS protein of Corpuscles
                                                                                                                                                                                                                                                                                                                                                        Length 75;
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  12; Indels
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                             309 GCTGTGACCTTTGAGGTGGCTGAGGCCCCGGTGCCCAGCATAC 351
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                                          14 CATCCCACCTGCAGGCTCCGTTCAGTGTTCTGGCCACGTCGG
                                                                                                                                                                                                                                                                                                                                                        DB 6;
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Pred. No. 2.6e+05;
1; Mismatches 15;
                                                                                                                                                                                                                                                                                    construct"
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Pred. No. 2.4e+05;
0; Mismatches 12
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Garen, A. and Cai, X.
Human monoclonal anti-tumor antibodies
Patent: US 6140470-A 45 31-OCT-2000;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45 from patent US 6140470.
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AR020462
                                                                                                                             75 bp
                                                                                                                                                                                                                                                                                    /organism="synthetic ( /db_xref="taxon:32630
                                                                                                                                                                                                                                                        Location/Qualifiers
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26 c 15 g
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                                                                                                                                                                                                                                                                                                                                                       1.6%;
ilarity 72.1%;
Conservative 0
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                                                                                                                                                                                                            synthetic construct.
synthetic construct
artificial sequences
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A05173.1 GI:345032
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Matches 32; Conserv
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AR020462/c
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AR117953/c
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A05173
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CIZNI5/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
C07K16/18,
                                                                                                                                                             The identification and integration of transcripts mapping to human chromosome 16p12.2 - p12.1 Unpublished
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 64)
                                                                           Direct Submission
Submitted (29-SEP-1997) Greenham J.A., Paediatrics, University
College London Medical School, The Rayne Institute, 5 Universit
Street, London., WCIE 6JJ, U.K
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Humanized anti-Fas antibody
Petent: JP 2000166574-A 105 20-JUN-2000;
SANKXO CO LTD
                                                                                                                                                                                                                                                                                                                              1 others
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Pred. No. 1.4e+05;
0; Mismatches 9;
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Pred. No. 2.3e+05;
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Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="pl2.2"
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/organism="synthetic con-
/db_xref="taxon:32630"
a 16 c 23 g ]
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Humanized anti-Fas antibody.
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JP 2000166574-A/105
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72.18;
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Best Local Similarity 76.9%;
Matches 30; Conservative
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Homo sapiens.
Homo sapiens
                                                                   Greenham, J.A.
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ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

AUTHORS

REFERENCE

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Antigens composed of major histocompatibility complex class I antigens and specific carrier molecules, their production and use Patent: EP 0352761-A 5 31-JAN-1990; BEHRINGWERKE Aktiengesellschaft
                                                                                                                                                                                                                                                                  Non-amidated derivatives of somatocrinine and process
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 CGGCIGCIGCAGGGITGCIGGGGCCCCCTCTICCIGCTIGGGTIGGCCC 303
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                                                                                                      Albu6/
Nucleotide sequence 8 from patent number EP0206863.
Al5067
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                        Score 23.4; DB 6;
Pred. No. 3.1e+05;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
/db_xref="taxon:32630"
27 c 25 g 7, t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 6;
Pred. No. 4e+05;
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/organism="unidentified"
/db_xref="taxon:32644"
a 21:c 24 g 13:
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                                                                                                                                                                                                                                                                                preparation by genetic engineering patent: EP 0206863-A 8 30-DEC-1986
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                                                                                                                                                                                                                                                      and Ferrara, P.
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Seemann, G., Bosslet, K.
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ilarity 67.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 71)
Gold, L., Jayasena, S.D., Nieuwlandt, D. and Davis, K.
High affinity oligonucleotide ligands to chorionic gonadotropin
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Drolet, D.W., Jayasena, S.D. and Gold, L.
Enzyme linked oligonucleotide assays (ELONAS)
Patent: US 5789163-A 2 04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.6; DB 6;
Pred. No. 2.7e+05;
                                                                                                                                                     Score 23.6; DB 6;
Pred. No. 2.7e+05;
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Patent: US 5837456-A 5 17-NOV-1998;
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AR054774
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16 c 33 q
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ilarity 69.6%;
Conservative
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BASE COUNT ORIGIN

Matches

AR066039/c.

DEFINITION

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REFERENCE AUTHORS

TITLE

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FEATURES

BASE COUNT ORIGIN

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Gaps

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PAT 19-JUL-1993

PAT 19-JUL-1993

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DEFINITION

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CBE345111 74 bp DNA circular PLN 04-JAN-2002 Carpinus betulus chloroplast microsatellite, ccmpl0 (3). AJ345111
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fagales; Betulaceae; Carpinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast DNA phylogeography of the hornbeam in Europe: evidence for a bottleneck at the outset of postglacial colonization
                                                                                               Synthetic construct
artificial sequences.

1 (bases 1 to 74)
Seemann, G., Bosslet, K. and Sedlacek, H.H.
Antigens composed of major histocompatibility complex class I
Patent: EP 0352761-A 031-JAN-1990;
BEHRINGWERKE Aktiengesellschaft
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Direct Submission
Submitted (18 SEP-2001) Grivet D., Recherches forestieres, Inra, BP45, Gazinet Cedex, 33611, FRANCE
Location/Qualifiers
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Pred. No. 4.5e+05;
0; Mismatches 22; Indels
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Pred. No. 4e+05;
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/db_xref="taxon:32630"
25 c 27 g 15 t
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/organism="Carpinus betulus"
/db_xref="taxon:12990"
synthetic oligonucleotide primer Vb.
A08224
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11 c 6 g
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st Local Similarity 68.1%;
Matches 32; Conservative
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Best Local Similarity 62.1%;
Matches 36; Conservative
                                                                                   synthetic construct.
                                                A08224.1 GI:413429
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other nucleic acid /desc = "Synthetic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SED ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 72 base pairs
7 TYPE: nucleic acid
7 STRANDEDNESS: single
7 TOPOLOGY: linear
7 MOLECULE TYPE: other nucle
7 DESCRIPTION: /desc = "S;
US-09-020-846-51
                                                                                                                      alignments)
Million cell updates/sec
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                                                                                                    October 31, 2002, 21:49:51; Search time 59 Seconds
                                                                                                                                                                                                                                                                                                                                662272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seg:*/cgn2_6/ptodata/1/ina/5B_COMB.seg:*
                                                                                                                      (without 7568.159 )
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-08-707-237A-26

-08-482-085B-55

5-08-475-411A-22

-08-478-029A-22

5-09-444-791A-55
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US-08-478-029A-23
US-09-444-791A-56
US-07-991-867B-29
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                                                                                                                                                                                                                                                                                                                             l number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-543-004-38
                                                                                                                                                                                                                                                                                            441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_NA:*
                                                                                                                                                                 US-09-919-197-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 75
                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                Minimum DB
Maximum DB
                                                                  OM nucleic
                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
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Sequence 29, Appl Sequence 29, Appl Patent No. 5438330 Sequence 173, Appl Sequence 21, Appl Sequence 21, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 21, Appl Sequence 2		
69 1 US-08-107-755A-29 69 2 US-08-544-332-29 69 4 US-09-70-861A-29 58 6 543633-3 61 1 US-08-055-39-4 75 4 US-09-042-353-173 71 2 US-08-648-402A-28 71 2 US-08-484-52A-28 71 2 US-08-484-52A-28 71 2 US-08-484-52A-28 71 2 US-08-484-52A-28 71 2 US-08-484-52A-28 71 2 US-08-441-376-26 74 2 US-08-412-376-26 75 4 2 US-08-412-376-26 76 4 US-09-412-376-26 77 4 US-09-412-376-26 78 5 PCT-US4-06079-39 70 4 US-09-08-353-172 70 4 US-09-08-353-172 70 4 US-09-08-411-A-20 75 4 US-09-08-411-A-20 76 4 US-09-08-411-A-20 77 4 US-09-08-411-A-20	ALIGNMENTS /C pplication US/09020846 2965 2965 XAMAGUCHI, Kenjiro KASHIWAKUMA, Tomiko CHIBA, Yukie AGI, Shintaro HASEGAWA, Akira VEWION: CHIMERA ANTIGEN PEPTIDE EQUENCES: 72 NCE ADDRESS: I. FOLEY & LARDNER 3000 K Street, N.W. Shington C. C	ION DATA: NUMBER: JP 9-027015 10 -FEB-1997 10 DATA: NUMBER: JP 8-024045 09-FEB-1996 11 FEB-1996 12 FEB-1996 13 FEB-1996 14 FEB-1996 15 FEB-1996 16 FEB-1996 17 FEB-1996 18 FEB-1997 18 FEB
28 22.2 1.5 330 22.2 1.5 331 22.2 1.5 332 22.2 1.5 334 22.2 1.5 334 21.8 1.5 34 21.8 1.5 36 21.8 1.5 37 21.8 1.5 38 21.6 1.5 41 21.6 1.5 42 21.6 1.5 43 21.6 1.5 44 21.4 1.5	1 1020-846-51/C ence 51, Applic ente 51, Applic nt No. 632296 ERAL INFORMATI PPLICANT: YASI ONERATING: YASI ON	PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 9 FILING DATE: 10 FEB-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 8 FILING DATE: 09 FEB-1996 ATTORNEY/AGENT INFORMATION: NAME: WEGISTRAFION NUMBER: 25,
00000 0 00	PESULT Seque Canal Can Canal Canal Canal Canal Canal Canal Canal Canal Canal Canal Can Canal Canal Canal Canal Ca Canal Canal Canal Canal Canal Canal	

Matches

RESULT 2

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HIGH AFFINITY OLIGONUCLECTIDE LIGANDS TO
CHORIONIC GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN
HORMONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.6; DB 1; Length 71; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     952 GCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 GTCGTCTGGCCAGTCCCCTCCACGCCCTCCACACTCAGCCCTT 18
                                   ENZYME LINKED OLIGONUCLEOTIDE ASSAYS
                                                                                                                                                                                                                                         COMPUTER READABLE FORM: 3 1/2 diskette, 1.44 MB MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All U's are 2'-NH2 uracil
                                                                                                                 E: Swanson & Bratschun, L.L.C.
8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 US/08/487,425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/234,997
FILING DATE: 28-APRIL-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/536,428
FILING DATE: 11-UNDE 1990
PRIOR APPLICATION DATA: 07/564,624
FILING DATE: 21-OCTOBER-1992
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
INFORMATION FOR SEQ ID NO; 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       WordPerfect 5.1
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Best Local Similarity 69.69
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GOLD ET AL.!
TITLE OF INVENTION: HIGH
TITLE OF INVENTION: GHOI
TITLE OF INVENTION: HORN
NUMBER OF SEQUENCES: 16C
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson &
JAYASENA, S
GOLD, LARRY
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
US-08-487-425-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inear
                       APPLICANT: GOLD, LA
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: RNA
                                                                                                                                                             Englewood
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-488-402A-5/c
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                                                                                                                                                                                  STATE: C
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                                                                                                                                          STREET:
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                                                                   Gaps
                                                                                                       1081 TGCTCAGGTGACCTGTTCCAGCCCAGGCAGAGATCAGGTGGGCAGAGGCTG 1131
                                                                                                                                70 TGCTCCGGTGACCTATTCCACCTACGGTAAATACCTGGCGGACGGCGGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 60;
                           Length. 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
                                                                 16; Indels
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                                                                                                                                                                                                                                                                                                        APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
CORRESPONDENCE: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.6; DB 3;
Pred. No. 1.3e+03;
1; Mismatches: 15;
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University STREET: 266 Whitney Avenue
                       Score 25.4; DB 4;
Pred. No. 4.4e+02;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer used in constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION 433
PRIOR APPLICATION DATA.
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE. June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MATY M. KTINESKY
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
                                                                                                                                                                                                                                               Sequence 45, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-487-425-2/c|
Sequence 2, Application US/08487425
Patent No. 5789163
GENERAL INFORMATION:
APPLICANT: DROLET, DAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: $ 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Processing CURRENT APPLICATION DATA:
                           1.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                             Query Match 1.73
Best Local Similarity 68.65
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Connecticut
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Matches 32; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: | linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06520-8114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Haven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DESCRIPTION:
US-08-983-607-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                   US-08-983-607-45/c
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STATE:

Query Match

RESULT 3

q δ

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952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
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                                                                                                     Diskette, 3 1/2 diskette, 1.44 MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All C's are 2'-NH2 modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: All U's are 2'-NH2 modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.6; DB 2;
Pred. No. 1.4e+03;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jayasena, Sumedha
APPLICANT: Gold, Larry
ITILE OF INVENTION: Method for Detecting a Targ
TITLE OF INVENTION: Compound in a Substance Usi
TITLE OF INVENTION: Nucleic Acid Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Swanson & Bratschun, L.L.C.
8400 E. Prentice Place, Suite 200
Englewood
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/964,624 FILING DATE: 21-OCTOBER-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/177,991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08628356A Patent No. 5874218
                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: 07/931,473
17-AUGUST-1992
                                                                                                                                                                                                                                                                                                                                         UMBER: 07/714,131
10-JUNE-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 8-SEPTEMBER-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NE)
                                                                                                                  COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                FILING DATE: 11-JUNE-1990.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drolet, Daniel W.
                                                                                                                                                             SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                       07 JUNE 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (303) 793-3433 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match . Best Local Similarity 69.65 Matches 32, Conservative
                                                                                                                                                                                CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-JUNE-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIÓR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                   APPLICATION NUMBER:
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                        Colorado
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                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                             USA
                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-484-552A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO CHORIONIC TITLE OF INVENTION: GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN HORMONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 23.6; DB 2; Length 71; 69.6%; Pred. No. 1.4e+03; tive 0; Mismatches 14; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   952 GCCGCCTGACCCGTGTCCTCCTCACGCCCTCCACCCTCAAGTCCAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GTGGTCTGGCCAGTCCCTCCACGTCCACACTCAGGCCCTT 18
                                                                                                                                      Diskette, 3 1/2 diskette, 1.44 MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All C's are 2'-NH2 modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: All U's are 2'-NH2 modified N8-488-402A-5
S: Swanson & Bratschun, L.L.C.
8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                           от June 1995
07 June 1995
07 June 1995
                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/488,40
FILING DATE: 07 JUNE 1995
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/931,473 FILING DATE: 17-AUGUST-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/964,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,991
FILING DATE: 8-SEPTEMBER-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08484552A
Patent No. 5849890
                                                                                                                                                         COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOLD, LARRY
JAYASENA, SUMEDHA
NIEUWLANDT, DAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: N
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TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160
                                                                                                                                                                                                                 URRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-AUGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10
                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAVIS, KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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                                       Englewood
                                                        Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-484-552A-5/C
ADDRESSEE:
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                                                                                                                                                                                                 SOFTWARE:
                                                                              COUNTRY:
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APPLICANT:
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                                                        STATE:
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Gaps

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Length 71 Indels

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HIGH AFFINITY OLIGONUCLEOTIDE
LIGANDS TO CHORIONIC GONADOTROPIN HORMONE AND RELATED
GLYCOPROTEIN HORMONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Swanson & Bratschun, L.L.C. 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.6; DE pred. No. 1.4e+0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: 08/488,402 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application PC/TUS9609472 GENERAL INFORMATION: APPLICANT: GOLD ET AL.
                                                                                                                                                       FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA: 7/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION NUMBER: 07/964,624
FILING APPLICATION TOWNER: 08/234,997
FILING DATE: 28-APRIL-1994
ATTORNEY AGENT INFORMATION:
NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
                                                      FILING DATE: 07-JUNE-1995
PRICR APPLICATION DATA:
APPLICATION NUMBER: 07/14,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
                                                                                                                                                                                                    07/964,624
                                                                                                                                                                                                                                                        08/234,997
                 PRIOR APPLICATION DATA: 08/487,425
APPLICATION NUMBER: 08/487,425
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                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%;
                                                                                                                                                                                                                                                                                                                                                                                       (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 69.6
Watches 32; Conservative
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TITLE OF INVENTION: GLY
NUMBER OF SEQUENCES: 16
CORRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: .71 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION:
PCT-US96-07439-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ENZYME LINKED OLIGONUCLEOTIDE TITLE OF INVENTION: ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.6; DB 2;
Pred. No. 1.4e+03;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Swanson & Bratschun, L.L.C.
8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All U's are 2'-amino uridine.
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                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,356A
FILING DATE: 05-APRIL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9607439 GENERAL INFORMATION:
                                                                                                                                                                           CHASSIFLATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: 24-MARCH-1995
FRIDK APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
                             MEDIUM TYPE: 3.5 inch disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/536,428 FILING DATE: 11-JUNE-1990
                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3 1/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytosine.
                                                                                                                                                                                                                                                                                                                                                                                                                      FELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
FORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DROLET, DAN
APPLICANT: JAYASENA, SUMEDHA
APPLICANT: GOLD, LARRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WordPerfect 6.0
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Best Local Similarity 69.6%;
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Barry J. Swanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
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ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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OTHER INFORMATION:
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                                                                                                                                             FILING DATE: 05
CLASSIFICATION:
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STREET: 84
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NAME:

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CURRENT APPLICATION NUMBER: US/09/425,638A
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CURRENT APPLICATION NUMBER: US/09/543,004
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09/425,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/609,716
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 38, Application US/09543004
Patent No. 6346249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-10-22
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69.8%;
                                                                                                                                                                                            1.5%;
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.5
Best Local Similarity 69.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER PRIOR FILING DATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 30; Conserv
                                        SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Car
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                                                                                                                                       ; FEATURE:
US-09-425-638A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                        RESULT 11.
US-09-543-004-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-543-004-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                    NUMBER OF SI
SEQ ID NO 38
                                                                          LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEO ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH
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LUD 5630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and APPLICANT: Lloyd J. Old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Church, Frank C.
APPLICANT: Bauman, Susannah J.
TITLE OF INVENTION: THROMBIN INHIBITORY AGENTS AND METHODS OF USING SAME FILE REFERENCE: 5470-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6%; Score 23.6; DB 5; Length 71; 69.6%; Pred. No. 1.4e+03; tive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 1.5%; Score 22.4; DB 4; Length 54; 1 Similarity 72.5%; Pred. No. 2.6e+03; 29; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:primer US-09-257-581-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GTCGTCTGGCCAGTCCCTCCACCTCCACACTCAGGCCCTT 18
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: All C's are 2'-NH2 modified
                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: All U's are 2'-NH2 modified US96-09472-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690 TAAATTACCTCCTCTAAAGGAGGAGGTAGTAGTGGGACCT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/257,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 60/076,210
EARLIER FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/09425638A
Patent No. 6342587
                                    08/484,552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      %3-09-257-581-1/c
; Sequence 1, Application US/09257581
: Patent No. 6207419
                                                                                        NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/48/
FILING DATE: 07 JUNE 1995
ATTORNEY/AGENT INFORMATION:
07 JUNE 1995
                                                                                                                                                                       TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
EQ ID NO 1
LENGTH: 54
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 32; Conserva
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Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt an APPLICANT: Lloyd J. Old
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                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
  Length 48;
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                                                          Indels
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Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 351101:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                               309 GCTGTGACCTTTGAGGTGGCTGAGGCCCCGGTGCCCAGCATAC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 GCTGTGACCTTTGAGGTGGCTGAGGCCCCGGTGCCCAGCATAC 351
                                                                                                                                                                       5 GATGGGCCCTTGGTGGAGGCTGAGGAGGGTGACCAGGGTGC 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22.2; DB 4;
Pred. No. 2.8e+03;
); Mismatches 13
Score 22.2; DB 4;
Pred. No. 2.8e+03;
); Mismatches 13
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Gaps

; 0

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APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W
APPLICANT: Dorman, Mary A
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 GGCAGCTGCCTCCCCAGGACCAGCGGCGGCTGCTGCAGGGTTGCTGGGGGCC 279
                                  229 GGCAGCTGCCTCCCCAGGACCAGGGCGGCTGCTGCAGGGTTGCTGGGGGCC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GCGAGAGCCGGGCGAGCTCCAGAACGGCTCCTGCACCACGCGGCACC 1
                                                        : Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22.2; DB 1;
Pred. No. 3.2e+03;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,801:
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/477,509B
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION: 22-APR-1993
PRILING DATE: 22-APR-1993
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-0CT-1987
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US 08/053,049
22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/175,155
FILLING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                         US-08-477-509B-55/c
Sequence 55, Application US/08477509B
Patent No. 5770697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                 Ferrari, Franco A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.5%;
Best Local Similarity 64,7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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    33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Four CITY: San Francisco cTAYE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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APPLICANT: Ferrari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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        Matches
                                                                                                                                           RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
APPLICANT: Dornan, Mary A.
TITLE OF INVENTION: Methods for Preparing Synthetic
TITLE OF INVENTION: Repetitive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,155 FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                                                            Score 22.2; DB 1;
Pred. No. 3.2e+03;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-55186-5/BIR
                                                                                                          A-55186-3/BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: (IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08175155
Patent No. 5641648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20015
                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                              ATTORNEY AGENT INFORMATION:
NAME: ROWLand, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A
                                                                                                                                                                                                                                                                                                                                                                  1.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
          06-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Rowland, Bertram REGISTRATION NUMBER: 20
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                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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EDNESS: single
                                                                                                                                                                                                                           LENGTH: 61 base pairs
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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st Local Similarity
tches 33; Conserva
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                              CLASSIFICATION:
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US-07-609-716-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111
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US-08-175-155-20/c
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qq

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RESULT 15

Length'61;

Score 22.2; DB 1; Pred. No. 3.2e+03;

1.5%;

Query Match Best Local Similarity

Length 61;

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US-80-10-213/A-26, Application US/08/0723/A
PREMEAL NO-98307104:
Sequence 26, Application US/08/0723/A
PREMEAL NO-98307104:
September 10-98307104:
STREET SOUR EMBERGAGE: 10-981
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Sequence 48, Appl Sequence 39, Appl Sequence 44, Appl Sequence 49, Appl Sequence 1130, Ap Sequence 5311, Ap

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Fatent No. US/20020025939A1
GENERAL INFORMATION:
TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
FILE REFERENCE: 0450-0026.30
CURRENT APPLICATION NUMBER: US/09/466,320
CURRENT APPLICATION NUMBER: US 60/112,910
EARLIER FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 73
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0 US-09-922-261-151

0 US-09-810-502-29

0 US-09-144-886-39

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0 US-09-988-899-49

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0 US-09-920-301-122

0 US-09-989-722-122

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Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: coding sequence US-09-466-320-16
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Patent No. US2020055095A1
GEMERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Matches 41; Conserv
                              246 GACCAG 251
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                                                 Query Match
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28813, A
758, App
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9, Appl
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Sequence 30, Appl
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                                                                                                                                                      October 31, 2002, 21:51:41; Search time 57 Seconds (without alignments) 8510.060 Million cell updates/sec
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/ Cgn2_6/ptodata1/pubpna/DS07_BNEW_PUB.seq:*
/ Cgn2_6/ptodata1/pubpna/US06_BNEW_PUB.seq:*
/ Cgn2_6/ptodata1/pubpna/US06_BUBW_BNES.
/ Cgn2_6/ptodata1/pubpna/US07_NEW_PUB.seq:*
/ Cgn2_6/ptodata1/pubpna/US08_BNEW_PUB.seq:*
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-944-036-30
US-09-919-580-637
US-09-790-11-7
US-09-787-574-8527
US-09-787-574-8527
US-09-783-590-2509
US-09-783-590-2509
US-09-874-547-8
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US-09-864-761-28813
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US-09-822-250-30
US-09-884-441-304
US-10-108-280-18
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US-09-975-408-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA:*
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                                                                                                              nucleic search, using sw model
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1456
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Match 1
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Gaps

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20.6 20.4 20.4 20.4 20.2 20.2

6 8 8 9 11 11 11 11 13

Score

Result No. 8.911 8.911 8.916 8.916 8.916

Gaps

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PPLICANT:

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TITLE OF INVENTION: Nucleic Acid Molecules and other Molecules Associated with TITLE OF INVENTION: Plants
FILE REFERENCE: 38-2(15401)
CURRENT PRICIATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1355 AAGCTTAGGCTGCTTATTGGACCAGAAGTCCTATCGACTTTATACAGAACTGAATTAAG 1413
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Pred. No. 1.1e+04;
0; Mismatches 24;
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9e+03;
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Pred. No. 9e+03
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
; ORGANIZM: Glycine max
; OTHER INFORMATION: Clone ID: 701101333H1:
US-09-878-574-8527
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8527, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/333,535 PRIOR FILING DATE: 1999-06-14
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Rhodes, Richard B.
Andrews, Christine A.
Hartnett, James R.
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Mandrekar, Michelle
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Best Local Similarity 59.3%;
Matches 35; Conservative
                                                                                                                                                                                                                                  1.4%;
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael
FILE REFERENCE: 1383.0210001
                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.3
Matches 33, Conservative
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Wood, Keith W.
                                                                                    SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 8527
LENGTH: 70
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                     CURRENT APPLICATION NUMBER CURRENT FILING DATE: 1999-
                                                               NUMBER OF SEQ ID NOS: 108
                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                        SEQ ID NO 7
LENGTH: 74
                                                                                                                                                  TYPE: DNA
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                                                                     APPLICANT: VERNET, GUY
FITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Capture (PTHER INFORMATION: Oligonucleotide 9-944-036-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Pyle, Ruth
APPLICANT: Yole, Ruth
APPLICANT: Xu Jiangchun
APPLICANT: Xu Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERENCE: 210121.552
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 64;
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65.2%; Pred. No. 8.2e+03;
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Pred. No. 7.6e+03;
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                                                                                                                       FILE REFERENCE; COLLORD OF CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/229,790 PRIOR FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 70 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 637, Application US/09919580 Patent No. US20020110832A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 56 |
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-637
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US-09-250-611-7/c
Sequence 7, Application US/09250611
Patent No. US20020143161A1
                                                                                                                                                                                                                                                                                                                              TYPE: DNA (
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%;
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APPLICANT: Byrne, Jennifer A.
APPLICANT: Basset, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                BABÖLA, Odile
TRAN, Nathalie
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Best Local Similarity
               BRENTANO,
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Matches 33; Conserv
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US-09-919-580-637/
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Matches

 0

Gaps

0

FEATURE:

PRIOR

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APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
ITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature
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US-09-783-590-3398
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                                                                                                                                                                                         INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                                                                                      INFORMATION: n equals a,t,g,
KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature
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APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
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56.6%;
                        PatentIn Ver. 2.0
    NUMBER OF SEQ ID NOS: 12485
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                                                                                                           ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
Matches 39; Conserva
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                        SOFTWARE: Pate
SEQ ID NO 2509
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LENGTH: 73
                                                                                         TYPE: DNA
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                                                                                                                                                                        CATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CANT: Rosen, Craig A.
CANT: Ruben, Steven M.
OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
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                                                                                                                                                                                                                                                                                                Length 55;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                            ; OTHER INFORMATION: target for mutant cytomegalovirus US-09-790-417-19
                                                                                                                                                                                                                                                                                            Score 20.4; DB 10;
Pred. No. 1.1e+04;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; OGGANISM: Glycine max
: OTHER INFORMATION: Clone ID: LIB3028-022-Q1-B1-D9
US-09-878-574-5162
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CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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CURRENT APPLICATION NUMBER: US/09/783,590
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; Sequence 2509, Application US/09783590
; Patent No. US20020110850A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5162, Application US/09878574 Patent No. US20020110548A1
APPLICATION NUMBER: 09/358,972
FILING DATE: 1999-07-21
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PRIOR FILING DATE: 1995-04-12
                                     APPLICATION NUMBER: 09/042,287
FILING DATE: 1998-03-13
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PRIOR FILING DATE: 1994-11-21
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APPLICANT: Haseltine, William A.
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ilarity 61.1%;
Conservative
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Best Local Similarity 61.1%;
tches 33; Conservative
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                                                                                NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                               TYPE: DNA ORGANISM: Cytomegalovirus
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Best Local Similarity
Matches 33; Conserva
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Gaps

APPLICANT: APPLICANT:

RESULT 8

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APPLICANT: APPLICANT:

APPLICANT

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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
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Pred. No. 1.7e+04;
0; Mismatches 19;
  10;
                                           415 CCCAGCCCTCCCTGGCTGCGGTGCAGTGGCTTCAAT 450
                                                                                14 cccagccagccardcccaagcrccagcrdcaacaar 49
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
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NAME/KEY: misc feature
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Patent No. US20020048763A1
                                                                                                                                                                                               Sequence 4790, Application US/09783590 Patent No. US20020110850A1
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Best Local Similarity 60.4%;
Matches 29; Conservative (
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Haseltine, William
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Rank, David R.
Hanzel, David K.
Chen, Wensheng
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    Conservative
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APPLICANT: Penn, Sh
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                                                                                                                                                            RESULT 12
US-09-783-590-4790/c
      26;
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APPLICANT:
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         Matches
                                                  QΥ
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
IITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
IITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
         1386 TATCGACTTTATACAGAACTGAATTAAGTTATTGATTTTGTAATAAAAGGTATGAAACA 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Primers for ScFv and Fab library generation (Table OTHER INFORMATION: 1) - MHV-Back5 US-09-874-547-8
                                                1394 TTATACAGAACTGAATTAAGTTATTGATTTTGTAATAAAAGGTATGAAACACTAAA 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 69;
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TITLE OF INVENTION: Screening of Phage Displayed Peptides
FITLE OF INVENTION: Without Clearing of the Cell Culture
FILE REFERENCE: 020144-0011100S
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/209,503
PRIOR FILING DATE: 2000-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: 50-LIB3058-032-01-K1-E6 US-09-983-965-3899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.2; DB 10;
Pred. No. 1.4e+04;
0; Mismatches '23;
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Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 05/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 3899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NOS: 84
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERGIA INFORMATION:
APPLICANT: No., US20020058269Alk, Steffen
APPLICANT: Kassner, Paul D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
                                                                                                                                                                                                                                                         Sequence 3899, Application US/09983965 Patent No. US20020137160A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-874-547-8 , cation US/09874547
equence 8, Application US/09874547
tent No. US2002005826941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.48;
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Best Local Similarity 59.6
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                         APPLICANT: Warren, Wesley C.
                                                                                                     1446 CTAAAAAAAA 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                 61 AAAAAAAAA 71
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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LENGIH: 69

FEATURE:

δλ ga. TYPE: DNA

NUMBER OF SOFTWARE:

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Score 19.8; DB 10;
Pred. No. 1.7e+04;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1421 TTTTTGTAATAAAGGTATGAAACACTAAAAAAAA 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n equals a,t,g, or c 09-925-301-758
RRENT FILING DATE: 2001-08-10
:IOR APPLICATION NUMBER: PCT/US00/05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/710,200
PRIOR FILING DATE: 2000-11-09
                                            PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09975408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nanogen, Inc.
APPLICANT: Weidenhammer, Blaine M.
APPLICANT: Xu, Xiao
APPLICANT: Kahl, Brenda F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n equals NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                            NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 758
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. US20020150917A1
                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (36)
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-975-408-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                    LOCATION
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                                                                                                                                                                                                                                                        FEATURE
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Pred. No. 1.7e+04;
0; Mismatches 15; Indels
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EST_HUMAN HIT: W45265.1, EVALUE 8.
NT HIT: X94232.1, EVALUE 6.00e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Annomax Sequence Listing Engine vers. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                              TLING DATE: 2000-09-27
PPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICATION NUMBER: PCT/US01/00663
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PPLICATION NUMBER: PCT/US01/00662
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PLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                         TLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                PPLICATION NUMBER: PCT/US01/00664
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ILING DATE: 2000-09-21
PPLICATION NUMBER: US 09/608,408
                                                                                  APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
                                                                                                                                                                                                                       PPLICATION NUMBER: US 60/236,359
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                                                                  FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                          LING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 65.9
Matches 29; Conservative
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Length 60;

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TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC FILE REFERENCE: 267/174 Patrick S. Eagleman CURRENT APPLICATION NUMBER: US/09/975,408
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                     Length 60;
                                                                                                                                                                                                                                                                                                                                                                 Score 19.8; DB 10;
Pred. No. 1.7e+04;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October 31, 2002, 23:19:53
Job time : 59 secs
                                                                                                                                                                                                                                                                                     1.4%;
                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.8
Matches 30; Conservative
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301

Sequence 758, Application US/09925301 Patent No. US20020052308A1

RESULT 14 US-09-925-301-758/c

g



1.8 53 14 H55352 1.8 35 14 R37139 1.8 55 9 A1123105 A	. 6 47 14 H97244 .8 46 9 AA916309 .7 61 12 BF581452 .7 63 10 AW333106 .7 47 14 N67514 .7 69 17 CNS0214K	1.7 65 17 1.7 74 9 1 1.7 64 9 1 1.7 61 9 1 1.7 67 10	1.7 75 14 NO8192 1.7 67 9 A1366713 1.7 73 9 AA987684 1.7 70 14, BQ454399 1.7 63 9 A1274192 1.7 71 14 T25646	24 1.6 64 9 AI448858 24 1.6 69 17 CNSOZI4K 24 1.6 72 9 AAB609 3.8 1.6 59 10 AW168138 3.8 1.6 65 9 AI897645	HSM011809 A1046959 AL675639 AL675639 AA785915 AA785915 A1468883 A1468883 R52050 R52050 H47793 A1250258 A1250258 A1250258	3.6 1.6, 72 10 AV948273 AV948273 AV948273 3.6 1.6 72 14 BQ394194 BQ394194 BQ394194 3.4 1.6 53 9 AA632173 AA6321	17/c A1221747 34 bp mRNA linear EST 30-NOV-1998 ION q993f02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842747 3' similar to TR:Q15466 Q15466 NUCLEAR HORMONE RECEPTOR; mRNA sequence. ON A1221747 A1221747 S1:3803950 S1:2803950	_	Tundr Gene Index Tundr Gene Lindex Tundr Gene Lindex Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Email: capabba-remail.nh.gov Email: capabba-remail.nh.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 990 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. RES 1. 34 /organism="Homo sapiens"
, o	c 112 c 133 c 144 16	17 c 19 c 20 c 21		C C C C C C C C C C C C C C C C C C C	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 444 0 445	RESULT 1 A1221747/C LOCUS DEFINITION ACCESSION VERSUON KEYWORDS	SOURCE ORGANISM ORGENISM REFERENCE AUTHORS TITLE	JOURNAL COMMENT FEATURES
			·	· · · · · · · · · · · · · · · · · · ·		• • • • • • • • • • • • • • • • • • • •			
*	Seconds s) cell updates/sec	a 1456						, G	1040-1040-1040-1040-1040-1040-1040-1040
5.1.3 Compugen Ltd.	; Search time 1937 Se (without alignments) 12173.789 Million cel	tatgaaacactaaaaaaaa	o lu.u , capext 1.u 1066 seqs, 8097743376 residues satisfying chosen parameters: 218680					results predicted by chance to have a to the result being printed	Descriptic A1221747 o B37921 HS B1745330 AA78923 a B1260363 BF632727

621

EST 25-SEP-2001

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AA782923 52 bp mRNA linear EST 05-FEB-1998 ai62c05.s1 Soares_testis_NHT HOMO Sapiens cDNA clone 1375400 3/ similar to 9b:X57025_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /hab_nostructed
/note="vector:_DAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
holversity, St. Louis. The CDNA was made by using Dynabead
Oligo-dT priming (Dynal). PCR based library using a
modified protocol from the SMART PCR CDNA Synthesis Kit
from Clontech, Directionally cloned into the UDG sites of
from the State University.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing-Center St. Louis.
                                                                                                                                                                                                                                                                                                                                                                                       McCarter, J., Cliffon, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, J., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tasgareishvili, R., Kennédy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Çardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                  Meloidogyne javanica
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Meloidogyne javanica egg pAMP1 v6 Chiapelii
                                                                                                                                                57 bp. mRNA linear EST 25-SEP-2
ranica egg pAMP1 v6 Chiapelli McCarter
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
The Washington University School of Medicine
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 1
Tel: 314 286 1810
Fax: 314 286 1810
565 TGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATTCATACCCAGGAAGCCT
                      Score 28.8; DB 13; Length 57;
Pred. No. 1.3e+04;
); Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Meloidogyne javanica"
/db_xref="taxon:6303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="enriched for eggs"
/lab_host="DH10B"
...
                                                                                                                                                                                    javanica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                    Meloidogyne javanica cDNA
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                                                                                                                                                                                    rk99b01.yl Meloidogyne
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                                                                                                                                                                                                                                                                                           root-knot nematode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 57)
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Matches 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
AA782923
                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                         RESULT 3
BI745330
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                                                         qq
                  Qγ
                                                                                                                                                                                         NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cohns from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 1.M.A.G.E. clones 297480-302087, subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS 18-OCT-1997
y C Homo
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                                                                                                           with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                       /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) v a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HS-1046-A2-G04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 829 Col=8 Row=M; DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 34;
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Pred. No. 7.5e+03;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
                                                                /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.4; DB 9;
Pred. No. 1.6e+03;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                     Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kzackron@u.washington.edu
Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               row: M column: 8
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                         2.2%;
ilarity 97.1%;
conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 616-8744
(206) 685-7301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.09
Best Local Similarity 70.29
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagged Connectors
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 62)
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Class: BAC ends
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34

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Matches

ORIGIN

RESULT 2 B37921/c

ACCESSION

KEYWORDS

REFERENCE AUTHORS

TITLE

FEATURES

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 52)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B1260363 72~bp mRNA linear EST 17-JUL-
602969412F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108786 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 72)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28.2; DB 9; Leuyur.
Pred. No. 1.9e+04;
                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                         cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LDNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                ww-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="137.5400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI260363.1 GI:14818593
AA782923.1 . GI:2842254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="male"
                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Conservative
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BI260363
                                                              Homo sapiens
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TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
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                                                                                                                                            AUTHORS
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BI260363
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Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Stores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula
bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                      /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1391 ACTTTATACAGAACTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAA 1450
                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27.6; DB 13; Length 72;
Pred. No. 2.7e+04;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                      /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11263 row: h column: 03
CDNA Library Preparation: Life Technologies, I
CDNA Library Arrayed by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
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High quality sequence stop: 72.
Location/Qualifiers
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/db_xref="taxon:3880"
/clone="nF046A08DT"
/clone_lib="brought"
/tissue_type="Plantlets"
                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                             /clone="IMAGE:5108786"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                            /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                    4
0
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BF632727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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BF632727/c
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                                                                                                                                                                                                                                                                M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                              Sequencing Center
information can be
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Gaps ö

Length 52;

EST 04-MAY-1995

40;

Matches

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Query Match Best Local S

SASE COUNT

AA 7

DEFINITION

LT 7

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL MEDLINE

COMMENT

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Email: est@watson.wustl.edu
Insert Size 1262
High quality sequence stops: 1
Source: IMAGE Consortium, ILNL This clone is available royalty-free
through LNL, contact the IMAGE Consortium (info@image.lln.gov)
for further information Trace considered overall poor quality
Insert Length: 1262 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yf54g11.s1 Soares infant brain 1NIB Homo sapiens CDNA clone
IMAGE:25970 3' similar to gb:X57025_rnal INSULIN-LIKE GROWTH FACTOR
IA PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through nor round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                       Mammalia; Euthéria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 35)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba;T., Le,M., Lennon,G., Marra,M., Parsons,J., Riklin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., W., Williamson,A., Wohldman,P. and Wilson,R.
                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI123105 5 bp mRNA linear EST 05-OCT qa85bl1.s1 Scares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1693533 3 similar to gb:x57025_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="IMAGE:25970"
/clone_lib="Soares infant brain lNIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26.2; DB 14;
Pred. No. 5.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. I 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCAGAGATTAAGTGACTTGCCCAAGGTCAC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAGAGGICAAGIGACTIGCCCAAGGICAC 34
                    35 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GDB:398317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo
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illarity 90.3%; l
Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:3538871
                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                              R37139.1 GI:794595
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                Homo sapiens
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Matches 28;
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R37139
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                REFERENCE AUTHORS
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                                                                                                          ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trofatter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F. and Buckler, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An expression-independent catalog of genes from human chromosome 22 Genome Res. 5 (3), 214-224 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E.coli DH5a" //lab_host="Red form human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into plusceriptIIKS+ at the Sal I and Bam HI sites."
                           entire
                                                                                                                                                                                                                                              1395 TATACAGAACTGAATTAAGTTATTGATTTTTTGTAATAAAGGTATGAAACACTAAAAAA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H55352 53 bp mRNA linear EST 07-DEC-
CHR220291 Chromosome 22 exon Homo sapiens cDNA clone C22_364 5'
                                                 plantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26.6; DB 14; Length 53;
Pred. No. 4.7e+04;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                       .
0
                             a mixture
                                                                                                                                                          Length 68;
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Massachusetts General Hospital
Bullding 149, 13th St., Charlestown MA 02129
                               /note="Vector: Lambda Zap; Contains
                                                                                                                                                          Score 26.8; DB 12;
Pred. No. 4.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="C22_364"
/clone_lib="Chromosome 22 exon"
         /dev_stage="Pooled timepoints"
                                                                                          46 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: buckler@helix.mgh.harvard.edu
                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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Conservative
                                                                                                                                                          1.8%;
                                                                        timepoints.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Buckler AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 53)
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 6177249616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 6177265736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nRNA sequence.
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EST 05-0CT-1998

Query Match

BASE COUNT

ORIGIN

sonrce

FEATURES

Local

Best Loca Matches

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RESULT 8

Gaps

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ORGANISM

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AUTHORS TITLE

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Control of the state of the sta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 47)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                             Email: est@watson wustl.edu
Insert Size: 2216
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Irace considered overall poor quality
Insert Length: 2216 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yv98e05.sl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:250784 3' similar to gb:X57025_rnal INSULIN-LIKE GROWTH
FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 26.2; DB 14; Length 60; 90.3%; Pred. No. 6.1e+04; 1ve 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares adult brain N2b4HB55Y"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GDB:3826840"
                                                                                                                                                                                                                                                                                                                     Insert Length; 2216 Std Erron
Seq primer: Promega -21m13
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:180196"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:1114287
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Matches 28; Conserv
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VERSION
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AUTHORS
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primer [5'
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1 (bases 1 to 60)
1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, T.R., Williamson, A., Wohldman, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a fort
                      Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 55)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                           National curve.

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26.2; DB 9; Length 55;
Pred. No. 6e+04;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 1038 Std Error: 0.00
Seq primer: -40013 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 CACAGAGGTCAAGTGACTTGCCCAAGGTCAC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone="IMAGE:1693533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 90.3%;
Conservative
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NbHL19W
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
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BASE COUNT

ORIGIN

Matches

EST 11.-DEC-1995

DEFINITION

LOCUS

JLT 10

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

Gaps 0

COMMENT

source

FEATURES

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Query Match
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ORIGIN
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source
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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BF581452
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                          High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image:llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1257 Std Error: 0.00
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                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25.8; DB 14; Length 47;
Pred. No. 7.4e+04;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:250784"
/clone_lib="Soares melanocyte 2NbHM"
                              Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAG 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AGAGGTTAAGNGACTTGCCCAAGGNCANACAG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sontact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                           Insert Length: 1257 Std Erron
Seg primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="GDB:3868490
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                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%;
milarity 84.4%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA916309.1 · GI:3055701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                  Tel:
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Best Local S
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BASE COUNT ORIGIN

Matches

δŏ g DEFINITION

ACCESSION

VERSION KEYWORDS

ULT 12 16309

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_GAAP_GEN] were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682652-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF581452 61 bp mRNA linear EST 12-DEC-2000 602100856F1 NCL_CGAP_CO24 Mus musculus cDNA clone IMAGE:4224253 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I Chases I to 61 in the sext of the content of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Greenlologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMggl3: row: p. column: 14
High quality sequence stop: 61.
High quality sequence stop: 61.
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                                                                                                                                     /clone_lib="Soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.8%; Score 25.6; DB 9; Best Local Similarity 87.5%; Pred. No. 8.3e+04; Matches 28; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAG 581.
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ordanism="Homo sapiens
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                                                                                         /clone="IMAGE:1561426"
                                 db_xref="taxon:9606"
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                                                                                                                                                                                                  /lab_host="DH10B
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BF581452
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EST 31-JAN-2000
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/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 47)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.

Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N6514 annual linear EST 08-MAF 2208910.s1 Soares melanocyte SNBHH whoo sapiens cDNA clone IMAGE:292002 3' similar to 9b.X57015_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                      AW333106 63 bp mRNA linear EST 31-JAN S17D5 AGS-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pneumocystis carinii f. sp. carinii"
/db_xref="taxon:38081"
/clone_lib="AGS-1"
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2 c 1 g 37 t
                                                         Score 25.4; DB 10; Length 63;
Pred. No. 9.7e+04;
0; Mismatches 11; Indels
                                                                                   Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 9.6e+04;
0; Mismatches 16
                                                                                                                                                                                                                                                                                                                              Pneumocystis carinii f. sp. carinii.
Pneumocystis carinii f. sp. carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: staben@pop.uky.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                    AW333106
AW333106.1 GI:6829463
Best Local Similarity 68.6%;
Matches - 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.48;
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Trel: 606 257 2161
Fax: 606 257 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Stabén C
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           Trevaskis, E., Waterston
                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
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                                                                      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 47;
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Rifkin, L., Rohlfing, T., Soares, m., Jan, T., Soares, m., Jan, T., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:292002"
/clone_lib="Soares melanocyte_2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25.2; DB 14;
Pred. No. 1.1e+05;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                       Seg primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /db_xref="GDB:3885132
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                         ,R., Williamson,A., Wohldmar
The WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.78;
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Best Local Similarity
Matches 27; Conservi
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Search completed: October 31, 2002, 23:17:17 Job time: 1941 secs

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